

Figure 1

CDR3

(39)

VS GGS NSG D Y Y W S W I R H P K G L DC G Y V Y S G S T Y Y N P L K S R V T I S V D I S K N O F L K L I S Y T A A D I A V Y Y C A R S T V N P G W E D P W G Q G T L V T Y S S (SEQ ID NO: 1)

CDR1

CDR2

Figure 2

G T C T C T G G T G G C T C C A T C A A C A G T G T G A T T A C T A C T G G A G C T G G A T C C G C A G C A C C C A G G G A A G G G C C T G A C T G C A T T G G G T A C A T C T A T T A C A G T G G A G C A C C T A C A C C C G T C C C T C A A G A G T C G A G T T A C C A T A C A G T A G A C A C G T C T A G A T C A G T T C T T C T G A A G C T G A C C T C T G T G A C T G C C G C G G A C A C G G C C G T C T A T T A C T G T G C G A G A T C T A C G T G G T A A T C C G G G G T G G T T C G A C C C T G G G G C C A R G G A A C C C T G T C A C C G T C T C A (SEQ ID NO: 2)

Figure 3

CDR3

(SEQ ID NO: 3)

T T T Q A S O D I N N Y L N W F O O K P K A P K Y L I H D A S N L E T G G P S R F S G S G S G I D E T E T I S G L O P E D I A T Y Y C O O Y E S L P L T F G G T K V E I K R T V A A P S V F I F P S D E Q (SEQ ID NO: 4)

CDR1

CDR2

Figure 4

A C C A T C A C T T G C C A G G C G A G T C A G A C A T T A M C A C T A T T T A A T T G G T T C A G C A G A A C C A G G A A A G C C C C T A A G G T C T G A T C C A G A T T T A C T T C A C C A T C A G C G G C C T G C A G C C T G A A G A C A T T G C A C A C A T A T T A T T G T C A A G A A C A G G G G G C C C A T C A A G G T T C A G A G A T T A C T G G A C A G A T T A C T T C G G C G G A G G A C C A A G G T G G A G A T C A A A (SEQ ID NO: 5)

CAGTATGAAA

(4)

Figure 5

VSQGSINSGDYYWSWIRHPRKGLIEWIGSIYYSGNTEYNPSISKRYTISLDTSKNOESLKLSVTAADTAVCYCARNITTCADFDWGGQGMVTYSS (SEQ ID NO: 7) 25
 CDR1 CDR2 CDR3 41

Figure 6

GTCCTGGTGGCTCCATCAA CAGTGGTGAT TACTACTGGA GCTGGATCCG CCAGCACCCA GGAAGGGCC TGGAGTGAT TGGTCCATC TATTACAGTG GGAACACCTT
 CTACAACCCG TCCCTCAAGA GTCGAGTTAC GATATCACTA GACACGCTTA AGAACAGATT CTCCTGAAG CTGAGTTCCTG TGAATGCCGC GGACACGGCC GTGTGTTACT
 GTGGAGAAA TATATGACT ACGGGTGCTT TTGATATCTG GGGCCAAAGG ACAATGGTCA CCGTCTCTTCA (SEQ ID NO: 8) 5

Figure 7

TTCQASODITLYLNWYOKRPGKAPKLLNDASSIETGVPLRSGSGSGTDFITISSLOREDIATVYCGOYDHLPLTGGGTVKAIKRTVAAPSVFRRPSPDEQ (SEQ ID NO: 9) 29
 CDR1 CDR2 CDR3 42

Figure 8

ACCATCACTT GTCAGGCGAG TCAGGACATT ACCATTATT TAAATTGTA TCAACAGAAA CCAGGAAAG CCCCT AAGTCTCTGA TCAACGACGC ATCCAGTTTG
 GAAACAGGGG TCCCATTAAG GTTCAGTGA AGTGATCTG GGACA GATTTTACTT TCACCATCAG CAGCTGCGAG CTTGAAGATA TTGCAACATA TTACTGTCAA
 CAGTATGATC ATCTC CCGTCACTT TCGGCGGCGG GACCAAGGTG GCGATCAAA (SEQ ID NO: 10) 6

Figure 9

VSGSISG **D**xyxw **L**wroHPGKGLHWIGYVYSGN **N**txyNPSL **K**SRV **S**MsIdTS **E**noPSL **K**LSSVTAAADIAVYYCARKPYTGGE **D**YWGQGTLVTVSS (SEQ ID NO: 14) **42**
CDR1 CDR2 CDR3 **43**

Figure 10

GTCTCTGTG GCTCCATCAG CAGTGGTGAT TACTACTGGA CCTGGAITCCG CCAGACACCA GGAAGGGCC TGGAGTGGAT TGGGTACATC TATTACAGTG GGAACACCTA
CTACAACCCG TCCTCAAGA GTGAGGTTTC CATGTCAATA GACACGCTCG AGAACCAAGT CTCCTGAAG CTGAGCTCTG TGACTGCCCG GGACACGGCC GTGTATTACT
GTGCGAGAAA ACCAGTGACT GGGGGGGAGG ACTACTGGGG CCAAGGAACC CTGGTCACCG TCTCTCA (SEQ ID NO: 15) **7**

Figure 11

TTTCASODISNYLNWYOOKPGKAPKLLIYDASNL **E**IGVPSRFSGSGGTIDTETITSSLOPHD **V**GyyVooY **E**SLPCGFGQGTKL **E**IKRTVAAPSVHPPSDHQ (SEQ ID NO: 16) **44**
CDR1 CDR2 CDR3 **44**

Figure 12

ACCATCACTT GCCAGGCGAG TCAGACATT AGTAACTATT TAAATTGTA TCAGCAGAAA CCAGGAAAG CCTAAGCTCCTGA TCTACGATGC TTCCAATTG GAAACAGGGG
TCCCATCAAG GTTCAGTGGA GTGATCTG GGACA GATTTACTT TCACCATCAG CAGCTGCAG CCTGAAGATG TTGAAACATA TGTCTGTCAA CAGTATGAGA GTCTC
CCGTCCGTT TTGGCCAGGG GACCAAACTG GAGATCAAA (SEQ ID NO: 16) **8**

Figure 13

VSGGSINSGDFFYMSWIROHPKGL⁵EWIGYXYSGSTYYNPSLKS²RVTM⁵IdP²SKNOFS²KL²ISTYAADTAVY²YCA²T²SL²YXGGMDYWGQGT²TVSS (SEQ ID NO: 16)

CDR1

CDR2

CDR3

Figure 14

GTCCTGTGTG GCTCCATCAA CAGTGGTGAT TTCTACTGGA GCTGGATCCG CCAACACCCA GGGAAAGGCC TGGAGTGAT TGGGTACATC TATTACAGTG GGAGCACC²TA
CTACAACCCG TCCCTCAAGA GTGAGATTAC CATGTCAATA GACCCGTCTA AGAACCAAGTT CTCCCTGAAA CTGATCTCTG TGA²CTGCCCG GGACACGGCC GTTATTACT²
GTGCGACNTC CCTTACTAT GGGCGGGGTA TGGACGICTG GGGCCAAGGG ACCACGCTCA CCGTCTCTC A (SEQ ID NO: 16)

Figure 15

TTTCQASODISNNLNWYOOKRG²NA²PKLL²YDASN²L²ITGVPSRSGSGSD²ETHIS²N²LOPED²IATYYCO²HYD²HL²PWTFGQGT²KVEX²KRT²V²AAPSV²FHP²PSDEQ (SEQ ID NO: 17)

CDR1

CDR2

CDR3

Figure 16

ACCATCACTT GCCAGGCGAG TCAGACATT AACAACTATT TGAATTGTA TCAGCAGAG CCNGGAACG CCCCT AAAC²TCTGA TCTACGATGC ATCCAATTG²
GAAACAGGGG TCCGATCAAG GTTCAGTGA AGTGATCTG GGACA GATTTACTT TCACCATCAA CAGCTGCAG C²TGAAGATA TTGGACATA TTA²TGTCAA²
CACTATGATC ATCTC CCGTGGACGT TCGCCAAAGG GACCAAGGTG GAANTCAA (SEQ ID NO: 18)

Figure 17

VSQGSINNDYYWSWROHPKGLFWGHHVYSGSTYLSLSKSLTISVDISKNOFSLKLNsvTAADIAVYYCARGIVLTYXEDYXWGGQCTTVTVSS (SEQ ID NO: 47)

CDR1 CDR2 CDR3

Figure 18

GTCTCTGGTGGCTCCATCAACAATGGTGTAT TACTACTGGA GCTGGATCCG CCAGACACCA GGAAGGGCC TGGAGTGGAT TGGGCACATC TATTACAGTGGAGCACCTA
CTACATCCCG TCCCTCAGA GTCGAACTAC CATATCAGTA GACACGTCTA AGAACCAAGT CTCCCTGAAG CTGAACCTCTG TGACTGCCCGG GACACAGGCC GTGTATTACT
GTGGAGAGG GACAGTAACT ACGTACTACT TTGACTACTG GGGCCAGGA ACCCTGGTCA CCGTCTCTC A (SEQ ID NO: 48)

Figure 19

TTTCRASQSSSYLNWYOOKPKGKAPKLLIYAASSLOSQGVPSRFSGSGSDTDELTTSSLOPEDFATYYCOOGYRTPPECSFGQGTKLKIRTVAAPSVFIFFPSDEQ (SEQ ID NO: 49)

CDR1 CDR2 CDR3

Figure 20

ACCATCACTT GCCGGGCAAG TCAGAGCAAT AGCAGCTAAT TAAATTGTA TCAGCAGAAA CCAGGGAAG CCCCT AAGCTCCTGA TCTATGCTGC ATCCAGTTTG
CAAAGTGGGG TCCCATCAAG GTTCAGTGGC AGTGATCTG GGACA GATTTCATCTC TCACCATCAG CAGTCTGCAA CCTGAAGATT TTGCAACTTA CTAAGTCA
CAGGTTACA GAACC CTCCGGAGT GCAGTTTGG CCAGGGGACC AAGCTGGAGA TCAAA (SEQ ID NO: 50)

12

48

Figure 21

VS~~GGSVSSG~~DYXWSWVROPKQLEWIGHLYXSGNITNYPSELKSKVTLSLDISKNOISLKLSVTAADTAVVYCA~~DEL~~IGSEPDYWGQGTILVTYSS (SEQ ID NO: 24)

CDR1

CDR2

CDR3

Figure 22

GTCCTGTGTG GCTCCGTCAG CAGTGTGTAT TACTACTGGA GCTGGATCCG GCAGCCCCA GGAAGGAGC TGGAGTGGAT TGGACATCTC TATTACAGTG GGAACACCAA
CTACAAACCCC TCCCTCAAGA GTCGAGTCAC CATATCATTA GACACGTCCA AGAACAGATT CTCCCTGAAG CTGACCTCTG TGACCGCTGC GGACACGGCC GTGTATTACT
GTGCGAGAGA TTTTITGACT GGTCCTCTTTGACTACTG GGGCCAGGGA ACCCTGGTCA CCGTCTCTC A (SEQ ID NO: 25)

Figure 23

TTTCASQDISNYLVNYYOORFKAPKLLNDASDLEHGVFSRISGSGGTD~~ET~~ETISNL~~OP~~EDIATYYCQOYDSLPLTFGGGTV~~VE~~IRRTVAAPSVFI~~PP~~SD~~EQ~~

CDR1

CDR2

CDR3

(SEQ ID NO: 26)

Figure 24

ACCATCATT GCCAGCGAG TCAGGACATA AGCAACTATT TAAATTGGTA TCAGCAGAAA CCAGGAAAAG CCCC~~T~~ AAGCTCCTGA TCAACGATGC ATCCGATTTG
GAAACAGGGG TCCCATCAAG GATCAGTGA AGTGAATCTG GGACA GATTTACTT TCACCATCAG CAACCTGCAG CCTGAGAGATA TTCAACATA TTACTGTCAA
CAATATGATA GTCTC CCGCTCATT TCGGCGGAGG GACCAAGGTG GAGATCAGA (SEQ ID NO: 27)

(14)

(13)

(49)

(50)

Figure 25

VSQGSV YSGD YXXWSW/HOPPGKGLIEWIGYDYSGSTNNPNSL KSRVTISVDISKNOFSI KLSVTAADTA VYYC ARDSIL GATIN YWGQGL VTVSS
CDR1 CDR2 CDR3

(SEQ ID NO: 30)

Figure 26

GTCTCTGGTGGTCTCCGCTCTA CAGTGGTGAT TACTACTGGA GCTGGATCCG GCAGCCCCC GGGAGGGGAC TGGAGTGAT TGGGTATATC TATTACAGTG GGAGCACC
TTACAATCCC TCCCTCAAGA GTCGAGTGAC CATATCAGTA GACACGTGCA AGAACAGATT CTCCCTGAAG CTGAGCTCTG TGACCGCTGC GGACACGGCC GTGTATTACT
GTGCGAGAGA CTCCATACTG GGAGCTACCA ACTACTGGGG CCAGGGAACC CTGGTCACCG TCTCTCA (SEQ ID NO: 31)

Figure 27

TTTCASO XISNYL XWYOOKPKAPK XLSDASNL ETGVPSRSGSGSGT XXTITISSLOPEDIA TYH CXOY XSLPLTGGG TKVEIKRTVAAPSVFI PPSDEQ
CDR1 CDR2 CDR3

(SEQ ID NO: 32)

Figure 28

ACCATCACTT GCCAGGCGAG TCNGGACATT AATACTATT TANATTGGTN TCAGCAGAAA CCAGGGAAG CCCCT AAATCTCTGA TCTCCGATCC ATCCAATT
GAAACAGGGG TCCCATCGAG GTTCAGTGA AGTGATCTG GGACA GANTINTACTT TCACCATCAG CAGCCTGCAG CCTGAAGATA TTGCNACATA TCACTGTCNA
CAGTATNATA GTCTC CCGCTCACTT TCGGCGGAGG GACCAAGTA GAGATCAAA (SEQ ID NO: 33)

116

52

51

15

Figure 29

VSGSVSSG D Y Y T Y R O S P G K G L E W I G H Y S G N T N N N S L K S R L T S I D I S K I O S L K S S V T A D T A L Y C V R D R V T G A D I W G Q T M V T S S (SEQ ID NO: 38)

CDR1

CDR2

CDR3

(53)

Figure 30

GTCCTGCTG GCTCCGTCAG CAGTGGTGAT TACTACTGGA CCTGGATCCG GCAGTCCCA GGAAGGAC TGGAGTGGAT TGGACACATC TATTACAGTG GGAACACCAA
TTATACCCC TCCCTCAAGA GTCGACTCAC CATATCAATT GACACGTCAC AGACTCAGTT CTCCCTGAAG CTGAGTTCTG TGACCGCTGC GGACACGGCC ATTATTACT
GTGTGCGAGA TCGAGTGACT GGTGCTTTTG ATATCTGGGG CCAAGGACA ATGGTCACCG TCTCTCA (SEQ ID NO: 39)

(17)

Figure 31

TTTCQASODISN N L N W Y O O K P G K A P K L L V D A S N L E I G V P S R F S G S G T I D T F T I S L O P E D I A T Y F C O H E D H L P A F G G G T K V E I K R T V A A P S V F I E P P S D E Q (SEQ ID NO: 40)

CDR1

CDR2

CDR3

(54)

Figure 32

ACCATCACTT GCCAGGCGAG TCAGGACATC AGCAACTATT TAAATTGGTA TCAGCAGAAA CCAGGAAAG CCCCT AAACCTCTGA TCTACGATGC ATCCAATTG
GAAACAGGGG TCCCATCAAG GTTCAGTGGA AGTGATCTG GGACA GATTTTACTT TCACCATCAG CAGCTGCAG CCTGAAGATA TTGCAACATA TTTCGTGCA CACTTTGATC
ATCTC CCGCTCGCTT TCGGCGGAGG GACCAAGGTG GAATCAAA (SEQ ID NO: 41)

(18)

10	20	30	40	50	
1234567890	1234567890	1234567890	1234567890	1234567890	
GCGATCCAGC	CTTTTAGGTC	CATGCCNTTC	TCCIGIGNAG	CGTCTGGATT	50
A I Q P	F R S	M P F	S C X A	S G F	
CCCCCTTCAGT	AGNINIGGCA	TGCACTGGGT	CCGCCAGGCT	CCAGGCAAGG	100
P F S	X X G M	H W V	R Q A	P G K G	
GCCTGGAGTG	GGTGGCAGTT	ATATGGTATG	ATGGAAGTAA	TAAATACTAT	150
L E W	V A V	I W Y D	G S N	K Y Y	
GCAGACTCCG	TGAAGGGCCG	ATTCAACATC	TCCAGAGACA	ATTCCAAGAA	200
A D S V	K G R	F T I	S R D N	S K N	
CACGCTGAT	CTGCAATGA	ACAGACTGAG	AGCCGAGGAC	ACGGCTGTGT	250
T L Y	L Q M N	R L R	A E D	T A V Y	
ATTACTGIGC	GACATTTTC	CAGTCCCTTC	CCCTTCAGTAA	CTCCCTTCAGTAA	300
Y C A	R F L	E W L P	F D Y	W G Q	
CCCTTCAGTAA	CTCCCTTCAGTAA	CTCCCTTCAGTAA	ACCAAGGGCC	CATCGGCTT	350
G T L V	T V X	S D S	T K G P	S V F	
CNCCCTGGCG	CCCTGCTTCC	AGGAGCACCC	TGNGANAGCA	CANANGGCCC	400
X L A	P C F Q	E H P	X X A	X X A P	
CTGGGACTGN	CTGNTACAAG	GACTINCTTC	CCTCNAACCN	GGTGACCNIN	450
G T X	X Y K	D X F P	S N X	V T X	
TCNIGGGAAA	CTCAGNGCNC	NICINNATNA	C		481
S W E T	Q X X	S X X			

(SEQ ID NO: 19)
(SEQ ID NO: 55)

20.1 heavy

10	20	30	40	50	
1234567890	1234567890	1234567890	1234567890	1234567890	
GGAACCTTIN	GGTTCGCNCC	TTTTGGAGNC	AGACCCANCA	TCACTTGTCTG	50
G T F X	F A P	F G X	R P X I	T C R	
GGCGAGTCAG	GGCATTAGCA	ATTTTTTAGC	CTGGTTTCAG	CAGAAACCAG	100
A S Q	G I S N	F L A	W F Q	Q K P G	
GGATAGCCCC	TAAGTCCCTG	ATCTATGCTG	CATCCACTTT	GCAAAGTGGG	150
I A P	K S L	I Y A A	S T L	Q S G	
GICCCATCAA	AGTTCACCGG	CAGTGGATAT	GGACAGATT	TCACTCTCAC	200
V P S K	F T G	S G Y	G T D F	T L T	
CATCAGCAGC	CTGCAGCCTG	AAGACTTTGC	AACTTATTAT	TGTCACAAT	250
I S S	L Q P E	D F A	T Y Y	C Q Q Y	
ATAATGTTTA	CCATTCACT	TTCGGCCCTG	GGACCAAAGT	GGATATCAAA	300
N V Y	P F T	F G P G	T K V	D I K	
CGAACTGTGG	CTGCACCATC	TGTCCTTCATC	TTCGCGCCAT	CTGATGAGCC	350
R T V A	A P S	V F I	F P P S	D E P	
AGTTGAAATC	TGGAAGTGGC	TCTGTGTGTG	GCCTGCTGAA	TAACTTCTAT	400
V E I	W N C L	C C V	P A E	. L L S	
CCCAGAGAGG	CCAAAGTACA	GIGGAAGGTG	GATAACGCCN	CNNTTGGCGG	450
Q R G	Q S T	V E G G	. R X	X W R	
NNICCTTTTIN	CTNCCCNIC	CTNCCCNIC	CTCTCNNA	(SEQ ID NO: 20) 489	
X P F X	X P S	S X X	L S X	(SEQ ID NO: 56)	

20.1 Kupper

10	20	30	40	50	
1234567890	1234567890	1234567890	1234567890	1234567890	
AAGCCTGTIG	CCTCAGTGCA	GGICTCCTGC	AAGGCTTCTG	GATACACCTT	50
K P V A	S V Q	V S C	K A S G	Y T F	
CACCAGTTAT	GATATCAACT	GGGTGCGACA	GGCCACTGGA	CAAGGGCTTG	100
T S Y	D I N W	V R Q	A T G	Q G L E	
AGTGGATGGG	ATGGATGAAC	CCTAACAGTG	GTAACACAGG	CTATGCACAG	150
W M G	W M N	P N S G	N T G	Y A Q	
AAGTTCAGG	GCAGAGTCAC	CATGACCAGG	AACACCTCCA	TAAGCACAGC	200
K F Q G	R V T	M T R	N T S I	S T A	
CTACATGGAG	CTGAGCAGCC	TGAGATCTGA	GGACACGGCC	GTTGATTACT	250
Y M E	L S S L	R S E	D T A	V Y Y C	
GTGCGAGAGG	AGGCCCCAT	AGCAGTGGCT	GGACCTTCTT	TGACTACTGG	300
A R G	G P Y	S S G W	T F F	D Y W	
GGCCAGGGAA	CCCTGGTCAC	CGTCTCCTCA	GCCCTTCACC	AAGGGCCCAT	350
G Q G T	L V T	V S S	A L H Q	G P I	
CGTCTTCCC	CCTGGCGCCC	TGCTCCAGGA	GCACCTCCCA	GAGCACANTC	400
G L P	P G A L	L Q E	H L P	E H X X	
NNCCCTGGG	CTGCCTGCNN	CAAGGACTCT	TTCCCCNAAC	CCCGGNTGA	449 (SEQ ID NO: 21)
P L G	C L X	Q G L F	P X T	P X	(SEQ ID NO: 57)

DNI

20.3 heavy

10	20	30	40	50	
1234567890	1234567890	1234567890	1234567890	1234567890	
TTTGAACCCCT TCNIGGCCCGT GTCTCTINGGC GCGAGGGCCA CCATCAACTG					50
F E P F X A V S L G A R A T I N C					
CAAGTCCAGC CAGCGTGTTC TATACANCTC CAACAATAAG AACTGCTTAG					100
K S S Q R V L Y X S N N K N C L A					
CTTGGTACCA GCAGAAACCA GGACAGCCTC CTAAGCTGCT CATTACTGG					150
W Y Q Q K P G Q P P K L L I Y W					
ACATCTACCC GCGAATCCGG GTTCCCTGCC CGATTCACTG GCAGCGGGTC					200
T S T R E S G V P A R F S G S G S					
TGGGACAGAT TTCACTCTCA CCATCAGCAG CCTGCAGGCT GAAGATGTGG					250
G T D F T L T I S S L Q A E D V A					
CAGTTTATTA CTGTACAGCA TATTATAGTA CTCCACTCAC TTTCGGGGGA					300
V Y Y C Q Q Y Y S T P L T F G G					
GGGACCATGG TGGAGATCAA GCGAAGTGTG GCTGCACCAT CTGTCTTCAT					350
G T M V E I K R T V A A P S V F I					
CTTCCCGCCA TCTGATGAGC CNGTINIGAAA TCTGGAACTG CCTCTGTTTG					400
F P P S D E P V . N L E L P L F V					
TGTTCCCTGC TGAATAACTT CTATCCAGCA GAGGCCAAAG TACCAGTGA					450
C P A E . L L S Q R G Q S T S G					
AGGTGGATAA (SEQ ID NO: 22)					460
R W I (SEQ ID NO: 58)					

20.3 kppen

10	20	30	40	50	
1234567890	1234567890	1234567890	1234567890	1234567890	
CNGCCTGTTA	GGTCCNIGCG	ACTCTCCTGT	GCAGCGICTG	GATTCATCTT	50
X P V R	S X R	L S C	A A S G	F I F	
CAGTACNTAT	GGCATGCACT	GGGTCCGCCA	GGCTCCAGGC	AAGGGGCTGG	100
S X Y	G M H W	V R Q	A P G	K G L E	
AGTGGGIGGC	AATTATATGG	TATGATGGAA	GTAATAAATA	CTATGCAGAC	150
W V A	I I W	Y D G S	N K Y	Y A D	
TCCGTGAAGG	GCCGATTCAC	CATCTCCAGA	GACAATTCOA	AGAACAGGCT	200
S V K G	R F T	I S R	D N S K	N T L	
GTATCTGCAA	ATGAACAGCC	TGAGAGCCGA	GGACACGGCT	GIGTATTACT	250
Y L Q	M N S L	R A E	D T A	V Y Y C	
GTCGAGAGA	CGGGGGGCCA	<u>CGGTGGTTTC</u>	TGCCTTCTGA	CTACTGGGGC	300
A R D	G G P	R W F L	A S D	Y W G	
CAGGGAACCC	TGGTCACCGT	CTCCTCAGCC	TCCACCAAGG	GCCCATCGGT	350
Q G T L	V T V	S S A	S T K G	P S V	
CTTCCCCCTG	GCGCCCTGCT	CCAGGAGCAC	CCTTCGAGAG	CACAGCGGCC	400
F P L	A P C S	R S T	L R E	H S G P	
CTGGGCTGCC	TGGTTCAGG	ACTACTTTCC	CCGAACCGGT	GACGGTGINC	450
G L P	G S R	T T F P	E P V	T V X	
GTGGAACTC	ATGAC	(SEQ ID NO: 23)			465
V G T H	D	(SEQ ID NO: 59)			

20.8.1 copy

10	20	30	40	50	
1234567890	1234567890	1234567890	1234567890	1234567890	
AGTCTCCAGA	CTCCCTGGTT	GIGICTCTGG	GCGAGAGGC	CACCATCAAC	50
S L Q T	P W L	C L W	A R G P	P S T	
TGCAAGTCCA	GNCAGAGTAT	TTTATACAGC	TCCAACAATC	AAAAACTTCT	100
A S P	X R V F	Y T A	P T I	K N F L	
TAGCTTGGTA	CCAGCAGAAA	CCAGGACAGC	CTCCGAAGTT	GCTCATTTAC	150
A W Y	Q Q K	P G Q P	P K L	L I Y	
TGGGCATCTA	TTCCGGGAATC	CGGGGTCCT	GACCGATTCA	GIGGCAGCG	200
W A S I	R E S	G V P	D R F S	G S G	
GTCCTGGACA	GATTTCACCTC	TCACCATCAG	CAGCCTGCAG	GCTGAAGATG	250
S G T	D F T L	T I S	S L Q	A E D V	
TGGCAGTTTA	TTACTGTCAG	CAGTATTATA	GTATTCGGTG	CACTTTGGC	300
A V Y	Y C Q	Q Y Y S	I P C	T F G	
CAGGGGACCA	AGCTGGAGAT	CAAACGAACT	GIGGCTGCAC	CATCTGICTT	350
Q G T K	L E I	K R T	V A A P	S V F	
CATCTTCCCG	CCATCTGATG	AGCAGTTGAA	ATCTGGAAGT	GCCTCTGTG	400
I F P	P S D E	Q L K	S G T	A S V V	
TGIGCCTGCT	GAATAACTTC	TATCCCAGAA	AGGCCAAAGT	ACATGAAGGG	450
C L L	N N F	Y P R K	A K V	H E G	
TTCAAA	(SEQ ID NO: 24)				456
F K	(SEQ ID NO: 60)				

20.8.1 Kupper

E20.11.2H Sequence

0 - 10p 30
D - DIR5
J - JH4b

63
Fig. 63

10	20	30	40	50	
1234567890	1234567890	1234567890	1234567890	1234567890	
GGCGTGGYCC	AGCCTGKGAG	GTCCTTGAGA	CTCTCCTGIG	CAGCGTCTGG	50
G V X Q	P X R	S L R	L S C A	A S G	
ATTCAYCTTC	AGTARCTATG	GCATGCACTG	GGTCCGCCAG	GCTCCAGGCA	100
F X F	S X Y G	M H W	V R Q	A P G K	
AGGGGCTGGA	GTGGGTGGCA	ATTATATGGT	ATGATGGAAG	TAGCAAATAC	150
G L E	W V A	I I W Y	D G S	S K Y	
TATGCAGACT	CCGIGAAGGG	CCGATTCAAC	ATCTCCAGAG	ACAATTCCAA	200
Y A D S	V K G	R F T	I S R D	N S K	
GAACACGCTG	TATCTGCAAA	TGAACAGCCT	GAGAGCCGAG	GACACGGCTG	250
N T L	Y L Q M	N S L	R A E	D T A V	
TGTATTACTG	TGCGAGAGAC	GGGGGGCCAC	GGTGGTTTCT	CGCTTCTGAC	300
Y Y C	A R D	G G P R	W F L	A S D	
TACTGGGGCC	AGGGAACCT	GGTCACCGTC	TCTCAGCCT	CCACCAAGGG	350
Y W G Q	G T L	V T V	S S A S	T K G	
CCCATCGGTC	TTCCCCCTGG	CGCCCTGCTC	CAGGAGCACC	TTCCGAGAGC	400
P S V	F P L A	P C S	R S T	F R E H	
ACAGCGGCCC	TGGGCTGCCT	GGTCAAGGAC	TACTTCCCCG	AAMCGGTGAC	450
S G P	G L P	G Q G L	L P R	X G D	
GGGTGCTGG	AATCAGGCG	CTCTGACCAG	NGGCGTGCAC	AATCCCAGC	500
G V V E	L R R	S D Q	X R A Q	F P A	
NGTCTINAAG	GTTGAAATCG	TAANGGTTCA	AA	(SEQ ID NO: 25)	532
V L K	V E I V	X V Q		(SEQ ID NO: 61)	

20.11.2. heavy

10	20	30	40	50	
1234567890	1234567890	1234567890	1234567890	1234567890	
ACTCAGTCTC	CAGACTCCCT	GGCTGTGTCT	CTGGGCGAGA	GGGCCACCAT	50
T Q S P	D S L	A V S	L G E R	A T I	
CAACTGCAAG	TCCAGCCAGA	GTGTTTTATA	CGGCTCCAAG	AATCAGAACT	100
N C K	S S Q S	V L Y	G S K	N Q N Y	
ACTTAGCTTG	GTACCAGCAG	AAACCAGGAC	AGCCTCCTAA	GCTGCTCATT	150
L A W	Y Q Q	K P G Q	P P K	L L I	
TACTGGGCAT	CTACCCGGGA	ATCCGGGGTC	CCTGACCGAT	TCAGGGGCAG	200
Y W A S	T R E	S G V	P D R F	R G S	
CGGGICTAGG	ACAGATTICA	CTCTCACCAT	CAGCAGCCTG	CAGGCTGAAG	250
G S R	T D F T	L T I	S S L	Q A E D	
ATGTGGCAGT	TTACTTCTGT	CACCAATATT	ATAGTACTOC	GTTGGACGTT	300
V A V	Y F C	H Q Y Y	S T P	W T F	
GGCCAAGGGA	CCAAGGTGGA	AATCAAACGA	ACTGTGGCTG	CACCATCTGT	350
G Q G T	K V E	I K R	T V A A	P S V	
CTTCATCTTC	CCGCCATCTG	ATGAGCAGTT	GAAATCTGGA	ACTGCCCTCTG	400
F I F	P P S D	E Q L	K S G	T A S V	
TTGTGTGCCT	GCTGAATAAC	TTGTATCCCA	GAAAGCCAAG	GACACGAAAG	450
V C L	L N N	L Y P R	K P R	T R K	
GTCANACCNA	CCC	(SEQ ID NO: 26)			463
V X P T		(SEQ ID NO: 62)			

20.11.2 Kappa

10	20	30	40	50	
1234567890	1234567890	1234567890	1234567890	1234567890	
CGIGATCCNC	CTGENTGGTC	CCTGAGACTC	TCCTGTGCAG	CGTCTGGATT	50
R D P P	G W S	L R L	S C A A	S G F	
CATCTTCANT	AACIATINCA	TGCACTGGGT	CCGCCAGGCT	CCAGGCAAGG	100
I F X	N Y X M	H W V	R Q A	P G K G	
GGCTGGAGTG	GGTGGCAATT	ATATGGTATG	ATGGAAGTAG	CAAATACTAT	150
L E W	V A I	I W Y D	G S S	K Y Y	
GCAGACTCCG	NGAAGGGCCG	ATTCACCATC	TCCAGAGACA	ATTCCAAGAA	200
A D S X	K G R	F T I	S R D N	S K N	
CACGCTGTAT	CTGCAAATGA	ACAGCCTGAG	AGCCGAGGAC	ACGGCTGATG	250
T L Y	L Q M N	S L R	A E D	T A D V	
TATTACTGIG	CGAGAGACCG	TTGGGCCACG	GTTGGCTTCTC	GCTTCTGACT	300
L L C	E R R	L G H G	G F S	L L T	
ACTGGNGCNC	AGGGCAACNC	TGNCINACCG	TNTTCCTCAN	CCCTINTACNC	350
T G A Q	G N X	X X P	X S S X	L Y X	
AAGGGCCNCC	ATTNGGTCTT	TCCCCCCTGG	NNNNCCTGCT	CNATGNNNCA	400
R A X	I X S F	P P G	X P A	X X X T	
CCCTINCGACA	NCNACAN	(SEQ ID NO: 27)			417
L R X	X X	(SEQ ID NO: 63)			

2018 heavy

10	20	30	40	50	
1234567890	1234567890	1234567890	1234567890	1234567890	
TTCGTTGGCTG TGTCTCTTGG CGAGAGGNCC ACCATCAACT GCAAGTCCAG					50
F V A V S L G E R X T I N C K S S					
CCAGAGTATT TTATACAGCT CCAACAATCA AAACCTCTTA GCTTGGTACC					100
Q S I L Y S S N N Q N F L A W Y Q					
AGCAGAAACC AGGACAGCCT CCGAAGTTGC TCATTTACTG GGCATCTATT					150
Q K P G Q P P K L L I Y W A S I					
CGGGAATCCG GGGTCCCTGA CCGATTCACT GGCAGCGGGT CTGGGACAGA					200
R E S G V P D R F S G S G S G T D					
TTTCACTCTC ACCATCAGCA GCTGTCAGGC TGAAGATGTG GCAGTTTATT					250
F T L T I S S L Q A E D V A V Y Y					
ACTGTCAGCA GTATTATAGT ATTCCGTTGCA CTTTGGCCA GGGGACCAAG					300
C Q Q Y Y S I P C T F G Q G T K					
CTGGAGATCA AACGAACCTGT GGCTGCACCA TCCTGCTTCA TCTTCCCGCC					350
L E I K R T V A A P S V F I F P P					
ATCTGATGAG CCAAGNITGA AAATCTGGAA CTGCTCTCTGT TGTTGTCCCT					400
S D E P X L K I W N C L C C V P C					
GCTTGAATAA CTTCTATCCC AGAGANGGCC AAAGTCCNGT GGAAGGTGGA					450
L N N F Y P R X G Q S P V E G G					
TAC	(SEQ ID NO: 28)				453
Y	(SEQ ID NO: 64)				

20.18 kypen

10	20	30	40	50	
1234567890	1234567890	1234567890	1234567890	1234567890	
CTCACCTGCA	CTGTCTCTGG	TGGCTCCATC	AGTAGTTACT	NTTGGAGNTG	50
L T C T	V S G	G S I	S S Y X	W X W	
GATCCGGCAG	CCCGNAGGGA	AGGGACTGGA	GTTGATTGGG	TGTTTCTATT	100
I R Q	P X G K	G L E	W I G	C F Y Y	
ACAGNCGGAG	CACCAACTAC	AACCCCTCCC	TNAAGAGTCA	TGTCACCATA	150
X G S	T N Y	N P S L	K S H	V T I	
TCAGTAGACA	CGTCCAAGAA	CCAGTTCTAC	NIGAAGCTGA	GCINTGTGAC	200
S V D T	S K N	Q F Y	X K L S	X V T	
CGNTGCCGAC	ACGGNCGNGA	ATAACTGNGC	NAGAGATAGG	GGAGNAGTGN	250
X A D	T X X N	N X A	R D R	G X V X	
NNTGGCNINC	TACTINTGACT	ACTGAGGCCA	GNGAACCNTG	GNTCACAGTA	300
W X X	T X T	T E A X	E P W	X T V	
ATCCNTAAGN	CTNNCAANCA	AANGNENCCC	AANGNGANAC	NINNCININC	350 (SEQ ID NO: 29)
I X K X	X X Q	X X P	X X X X	X X	(SEQ ID NO: 65)

20.19.2 hang

10	20	30	40	50	
1234567890	1234567890	1234567890	1234567890	1234567890	
TCTTTGGTAG	CGNGTCTTGG	CGAGAGGCC	ACCATCAACT	GCAAGTCCAG	50
S L V A	X L G	E R P	T I N C	K S S	
CCAGAGTGT	TTATACNGCT	CCAAGAATCA	GAAGTACTTA	GCTTGGTACC	100
Q S V	L Y X S	K N Q	N Y L	A W Y Q	
AGCAGAAACC	AGGACAGCCT	CCTAAGCTGC	TCATTTACTG	GGCATCTACC	150
Q K P	G Q P	P K L L	I Y W	A S T	
CGGGAATCCG	GGGTCCCTGA	CCGATTCAGG	GGCAGCGGGT	CTAGGACAGA	200
R E S G	V P D	R F R	G S G S	R T D	
TTTCACTCTC	ACCATCAGCA	GCCTGCAGGC	TGAAGATGTG	GCAGTTTACT	250
F T L	T I S S	L Q A	E D V	A V Y F	
TCTGTCACCA	ATATTATAGT	ACTCCGIGGA	CGTTCGGCCA	AGGGACCAAG	300
C H Q	Y Y S	T P W T	F G Q	G T K	
GTGGAATCA	AACGAACTGT	GGCTGCACCA	TCTGTCTTCA	TCTTCCCGCC	350
V E I K	R T V	A A P	S V F I	F P P	
ATCTGATGAG	CACCTTGAAA	TTCTGGAAGT	GCCTCTGNTG	NGTGCTGCT	400
S D E	H L E I	L E L	P L X	X A C .	
GAACNAACTC	TATCCCCAGA	GANGGCCCAA	AAGINTCAAG	NINGNNAGGC	450
T N S	I P R	X G P K	V S X	X X G	
NINGATAACGC	CINTTNCN	NCNINC	(SEQ ID NO: 30)		476
X I T P	X X X	X	(SEQ ID NO: 66)		

20.19.2 Kuyppa

69
Fig. 69

10	20	30	40	50	
1234567890	1234567890	1234567890	1234567890	1234567890	
AAGCCTTTTC	AGACCNIGCC	CTTCACCTGC	ACTGTCCTCTG	GTTGGCTCCAT	50
K P F Q	T X P	F T C	T V S G	G S I	
CAGCAGTGGT	GGTTACTACT	GGAGCTGGAT	CCGCCAGCAC	CCAGGGAAGG	100
S S G	G Y Y W	S W I	R Q H	P G K G	
GCCTGGAGTG	GATTGGGTAC	ATCTATAACA	GTTGGGAGCAC	CTACTACAAC	150
L E W	I G Y	I Y N S	G S T	Y Y N	
CCGTCCCTCC	AGAGTCGAGT	TACCATATCA	GTAGACACGT	CTAAGAACCA	200
P S L Q	S R V	T I S	V D T S	K N Q	
GTCTCCCTTG	AAGCTGAGCT	CTGTGACTGC	CCGGGACACG	GCCGTGTATT	250
F S L	K L S S	V T A	A D T	A V Y Y	
ACTGTGCGGG	<u>TCAGAAATGG</u>	TCCTACTACT	ACTACTACGG	TATGGACGTC	300
C A G	Q K W	S Y Y Y	Y Y G	M D V	
TGGGGCCAAG	GGACCACGGT	CACCGTCTCC	TNAGCCTCCA	CCAANGGCCC	350
W G Q G	T T V	T V S	X A S T	X G P	
ATCGGTCTTC	CCCCTGGGCG	CCTGNTCTAG	GAGCACCTCC	CANAGCACAG	400
S V F	P L A P	X S R	S T S	X S T D	
ACGGATNCTG	GGCCTGCCTG	NATCAATGGA	CTACTTTCCC	CGAACCGGTT	450
G X W	A C L	X Q W T	T F P	E P V	
GNNIGTGNNN	CCTGGNAACT	N	(SEQ ID NO: 31)		471
X C X X	W X L		(SEQ ID NO: 67)		

20.21 heavy

Fig. 70

10	20	30	40	50	
1234567890	1234567890	1234567890	1234567890	1234567890	
AAGCCTTTTG	AGACCNFGCC	CCTCACCTGC	ACTGTCTCTG	GIGGCTCCAT	50
K P X E	T X P	L T C	T V S G	G S I	
CAGTAATTAC	TACTGGAGCT	GGATCCGGCA	GCCCCCAGGG	AAGGGACTGG	100
S N Y	Y W S W	I R Q	P P G	K G L E	
AGTGGATTGG	GIATATCTAT	TACAGTGGGA	GCACCAACTA	CAACCCCTCC	150
W I G	Y I Y	Y S G S	T N Y	N P S	
CTCAAGAGTC	GAGTCACCAT	ATCAGTAGAC	ACGTCCAAGA	ACCAGTCTTC	200
L K S R	V T I	S V D	T S K N	Q F S	
CCIGAAGCTG	AGCTCTGTGA	CCGCTGCGGA	CACGGCCGTG	TATTACTGTG	250
L K L	S S V T	A A D	T A V	Y Y C A	
CGAGAGGGCC	CGGGGGGAGC	TACTACTACT	ACGGTATGGA	CGTCTGGGGC	300
R G P	G G S	Y Y Y Y	G M D	V W G	
CAAGGGACCA	CGGTACCGT	CTCCTCAGCC	TCCACCAAGG	GCCCATCGGT	350
Q G T T	V T V	S S A	S T K G	P S V	
CTTCCCCCTG	GCGCCCTGCT	CCAGGAGCAC	CTCCGAGAGC	ACAGCGGCCC	400
F P L	A P C S	R S T	S E S	T A A L	
TGGGCTGCCT	GGGICAAGGA	CTACTTCCCC	GAACCGGTGA	CGGTGTTCCN	450
G C L	G Q G	L L P R	T G D	G V R	
NGGAAC	(SEQ ID NO: 32)				456
X N	(SEQ ID NO: 68)				

20.22 heavy

E7.5.2.K.aa Sequence

Figure 72

10	20	30	40	50	
1234567890	1234567890	1234567890	1234567890	1234567890	
CTGTCGTCAT	CTGTAGGACA	CAGAGTCATA	ATCACTTGCC	GGGCAAGTCA	50
L S A S	V G D	R V I	I T C R	A S Q	
AAACATCACC	GACCATTTAA	ATTGGTATCA	GCAGATAGCA	GGAAAAGCCC	100
N I T	D H L N	W Y Q	Q I A	G K A P	
CTAGGCCCCCT	GATATACACT	GCATCCAGTT	TGCAAGGTGG	GGTCCCATCA	150
R P L	I Y T	A S S L	Q G G	V P S	
AGGTTGAGTG	GCAGTGGATC	TGGGACAGAT	TTCACTCTCA	CCATCAGCAG	200
R F S G	S G S	G T D	F T L T	I S S	
TCTGCAACCT	GAAGATTTTT	CAACTTACTA	CTGTCAACAG	AGTTACAGTA	250
L Q P	E D F S	T Y Y	C Q Q	S Y S T	
CCCCGTGCAG	TTTGGGCCAG	GGGACCAAGC	TGGAGATCAA	ACGAACTGTG	300
P C S	F G Q	G T K L	E I K	R T V	
GCTGCACCAT	CTGTCCTTCAT	CTTCCCGCCA	TCTGATGAGC	AGTTGAAATC	350
A A P S	V F I	F P P	S D E Q	L K S	
TGGAAC TGCC	TCTGTTGTGT	GCCTGCTGAA	TAACTTCTAT	CCCA	394 (SEQ ID NO: 33)
G T A	S V V C	L L N	N F Y	P	(SEQ ID NO: 69)

7.5.2 heavy

10	20	30	40	50	
1234567890	1234567890	1234567890	1234567890	1234567890	
GIGAAGGICT	CCTGCAAGGC	TTCTGGATAC	ACCTTCAGCG	GCTACTATAT	50
V K V S	C K A	S G Y	T F S G	Y Y M	
GCACTGGGTG	CGACAGGCC	CTGGACAAGG	GCTTGAGTGG	ATGGGATCGA	100
H W V	R Q A P	G Q G	L E W	M G S I	
TCCACCCCTAA	CAGTGGTGGC	ANAAACTTTG	CACAGAAGTT	TCAGGGCAGG	150
H P N	S G G	X N F A	Q K F	Q G R	
GTCACCATGA	CCAGGGACAC	GTCCATCAAC	ACAGCCTACT	TGGAGCTGAG	200
V T M T	R D T	S I N	T A Y L	E L S	
CAGGCTGAGA	TCTGACGACA	CGGCCGTGTA	TTACTGTGCG	AGAGATAAAA	250
R L R	S D D T	A V Y	Y C A	R D K N	
ACTACGGTGA	CTACGTCTTT	GACTATTGGG	GCCAGGGAAC	CCTGGTCACC	300
Y G D	Y V F	D Y W G	Q G T	L V T	
GTCTCTCAG	(SEQ ID NO: 34)				310
V S S	(SEQ ID NO: 70)				

7.5.2kappa